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Reviewer: Durreshwar Anjum
Timestamp: [year=2011; month=1; day=10; hr=14; min=45; sec=3; ms=43;]
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Application No: 10697720   Version No: 3.0

Input Set:

Output Set:

Started:	2011-01-10 10:47:08.132
Finished:	2011-01-10 10:47:10.107
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 975 ms
Total Warnings:	21
Total Errors:	0
No. of SeqIDs Defined:	21
Actual SeqID Count:	21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-01-10 10:47:08.132

Finished: 2011-01-10 10:47:10.107

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 975 ms

Total Warnings: 21

Total Errors: 0

No. of SeqIDs Defined: 21

Actual SeqID Count: 21

Error code	Error Description
	This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (21)

<210> 1
<211> 1448
<212> DNA
<213> Artificial Sequence

<220>
<223> TSG101 nucleotide

<221> CDS
<222> (61)...(1203)

<400> 1
cccctctgcc tgtggggacg gaggagcgcg ccatggctgt ccgagagtca gctgaagaag 60
atg atg tcc aag tac aaa tat aga gat cta acc gtc cgt caa act gtc   108
Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
 1   5   10   15

aat gtc atc gct atg tac aaa gat ctc aaa cct gta ttg gat tca tat   156
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
            20   25   30

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gtt ttt aat gat ggc agt tcc agg gag ctg gtg aac ctc act ggt aca    204
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
         35                  40                  45

atc cca gtg cgt tat cga ggt aat ata tat aat att cca ata tgc ctg    252
Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu
     50                  55                  60

tgg ctg ctg gac aca tac cca tat aac ccc cct atc tgt ttt gtt aag    300
Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
 65                  70                  75                  80

cct act agt tca atg act att aaa aca gga aag cat gtg gat gca aat    348
Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
                 85                  90                  95

ggg aaa atc tac cta cct tat cta cat gac tgg aaa cat cca cgg tca    396
Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
                100                 105                 110

gag ttg ctg gag ctt att caa atc atg att gtg ata ttt gga gag gag    444
Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
         115                 120                 125

cct cca gtg ttc tcc cgg cct act gtt tct gca tcc tac cca cca tac    492
Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
     130                 135                 140

aca gca aca ggg cca cca aat acc tcc tac atg cca ggc atg cca agt    540
Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
145                 150                 155                 160

gga atc tct gca tat cca tct gga tac cct ccc aac ccc agt ggt tat    588
Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
                165                 170                 175

cct ggc tgt cct tac cca cct gct ggc cca tac cct gcc aca aca agc    636
Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
                180                 185                 190

tca cag tac cct tcc cag cct cct gtg acc act gtt ggt ccc agc aga    684
Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
         195                 200                 205

gat ggc aca atc agt gag gac act atc cgt gca tct ctc atc tca gca    732
Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
         210                 215                 220

gtc agt gac aaa ctg aga tgg cgg atg aag gag gaa atg gat ggt gcc    780
Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
225                 230                 235                 240

cag gca gag ctt aat gcc ttg aaa cga aca gag gaa gat ctg aaa aaa    828
Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
                245                 250                 255
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ggc cac cag aaa ctg gaa gag atg gtc acc cgc tta gat caa gaa gta      876
Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
            260                 265                 270

gct gaa gtt gat aaa aac ata gaa ctt ttg aaa aag aag gat gaa gaa      924
Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
        275                 280                 285

cta agt tct gct ctg gag aaa atg gaa aat caa tct gaa aat aat gat      972
Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
     290                 295                 300

att gat gaa gtt atc att ccc aca gcc cca ctg tat aaa cag att cta      1020
Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
305                 310                 315                 320

aat ctg tat gca gag gaa aat gct att gaa gac act atc ttt tac ctt      1068
Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
                325                 330                 335

gga gaa gct ttg cgg cgg gga gtc ata gac ctg gat gtg ttc ctg aaa      1116
Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
            340                 345                 350

cac gtc cgc ctc ctg tcc cgt aaa cag ttc cag cta agg gca cta atg      1164
His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
        355                 360                 365

caa aag gca agg aag act gcg ggc ctt agt gac ctc tac tgacatgtgc      1213
Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
     370                 375                 380

tgtcagctgg agaccgacct ctccgtaaag cattcttttc ttcttctttt tctcatcagt  1273
agaacccaca ataagttatt gcagtttatc attcaagtgt taaatatttt gaatcaataa  1333
tatattttct gtttcctttg ggtaaaaact ggcttttatt aatgcacttt ctaccctctg  1393
taagcgtctg tgctgtgctg ggactgactg ggctaaataa aatttgttgc ataaa       1448


<210> 2
<211> 381
<212> PRT
<213> Artificial Sequence

<220>
<223> TSG101 nucleotide

<400> 2
Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
 1               5                   10                  15
Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
            20                  25                  30
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
        35                  40                  45
Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu
    50                  55                  60
Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65                  70                  75                  80
Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
```

Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
                100   105   110
Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
            115   120   125
Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
        130   135   140
Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
145   150   155   160
Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
                165   170   175
Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
            180   185   190
Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
        195   200   205
Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
    210   215   220
Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
225   230   235   240
Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
                245   250   255
Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
            260   265   270
Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
            275   280   285
Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
        290   295   300
Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
305   310   315   320
Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
                325   330   335
Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
            340   345   350
His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
        355   360   365
Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
    370   375   380

<210> 3
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> TSG101 nucleotide

<400> 3
gaagggtgtg cgattgtgtg ggacggtctg gggcagccca gcagcggctg accctctgcc 60
tgcggggaag ggagtcgcca ggcggccgtc atggcggtgt cggagagcca gctcaagaaa 120
atggtgtcca agtacaaata cagagaccta actgtacgtg aaactgtcaa tgttattact 180
ctatacaaag atctcaaacc tgttttggat tcatatgttt ttaacgatgg cagttccagg 240
gaactaatga acctcactgg aacaatccct gtgccttata gaggtaatac atacaatatt 300
ccaatatgcc tatggctact ggacacatac ccatataatc cccctatctg ttttgttaag 360
cctactagtt caatgactat taaaacagga aagcatgttg atgcaaatgg gaagatatat 420
cttccttatc tacatgaatg gaaacaccca cagtcagact tgttggggct tattcaggtc 480
atgattgtgg tatttggaga tgaacctcca gtcttctctc gtcctatttc ggcatcctat 540

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ccgccatacc aggcaacggg gccaccaaat acttcctaca tgccaggcat gccaggtgga 600
atctctccat acccatccgg ataccctccc aatcccagtg gttacccagg ctgtccttac 660
ccacctggtg gtccatatcc tgccacaaca agttctcagt acccttctca gcctcctgtg 720
accactgttg gtcccagtag ggatggcaca atcagcgagg acaccatccg agcctctctc 780
atctctgcgg tcagtgacaa actgagatgg cggatgaagg aggaaatgga tcgtgcccag 840
gcagagctca atgccttgaa acgaacagaa gaagacctga aaaagggtca ccagaaactg 900
gaagagatgg ttacccgttt agatcaagaa gtagccgagg ttgataaaaa catagaactt 960
ttgaaaaaga aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtctgaa 1020
aacaatgata tcgatgaagt tatcattccc acagctccct tatacaaaca gatcctgaat 1080
ctgtatgcag aagaaacgc tattgaagac actatctttt acttgggaga gccttgaga 1140
agggggcgtga tagacctgga tgtcttcctg aagcatgtac gtcttctgtc ccgtaaacag 1200
ttccagctga gggcactaat gcaaaaagca agaaagactg ccggtctcag tgacctctac 1260
tgacttctct gataccagct ggaggttgag ctcttcttaa agtattcttc tcttcctttt 1320
atcagtaggt gcccagaata agttattgca gtttatcatt caagtgtaaa atattttgaa 1380
tcaataatat attttctgtt ttcttttggt aaagactggc ttttattaat gcactttcta 1440
tcctctgtaa acttttgtg ctgaatgttg ggactgctaa ataaaatttg tttt        1494
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<210> 4
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
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Met Ala Val Ser Glu Ser Gln Leu Lys Lys Met Val Ser Lys Tyr Lys
  1               5                  10                  15
Tyr Arg Asp Leu Thr Val Arg Glu Thr Val Asn Val Ile Thr Leu Tyr
             20                  25                  30
Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr Val Phe Asn Asp Gly Ser
         35                  40                  45
Ser Arg Glu Leu Met Asn Leu Thr Gly Thr Ile Pro Val Pro Tyr Arg
     50                  55                  60
Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu Trp Leu Leu Asp Thr Tyr
 65                  70                  75                  80
Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys Pro Thr Ser Ser Met Thr
                 85                  90                  95
Ile Lys Thr Gly Lys His Val Asp Ala Asn Gly Lys Ile Tyr Leu Pro
            100                 105                 110
Tyr Leu His Glu Trp Lys His Pro Gln Ser Asp Leu Leu Gly Leu Ile
         115                 120                 125
Gln Val Met Ile Val Val Phe Gly Asp Glu Pro Pro Val Phe Ser Arg
     130                 135                 140
Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln Ala Thr Gly Pro Pro Asn
145                 150                 155                 160
Thr Ser Tyr Met Pro Gly Met Pro Gly Gly Ile Ser Pro Tyr Pro Ser
                 165                 170                 175
Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro Gly Cys Pro Tyr Pro Pro
             180                 185                 190
Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser Gln Tyr Pro Ser Gln Pro
         195                 200                 205
Pro Val Thr Thr Val Gly Pro Ser Arg Asp Gly Thr Ile Ser Glu Asp
     210                 215                 220
Thr Ile Arg Ala Ser Leu Ile Ser Ala Val Ser Asp Lys Leu Arg Trp
225                 230                 235                 240
Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala Leu
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Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly His Gln Lys Leu Glu Glu
          260   265   270
Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys Asn Ile
          275   280   285
Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu Ser Ser Ala Leu Glu Lys
      290   295   300
Met Glu Asn Gln Ser Glu Asn Asn Asp Ile Asp Glu Val Ile Ile Pro
305   310   315   320
Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn Leu Tyr Ala Glu Glu Asn
                    325   330   335
Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly Glu Ala Leu Arg Arg Gly
          340   345   350
Val Ile Asp Leu Asp Val Phe Leu Lys His Val Arg Leu Leu Ser Arg
          355   360   365
Lys Gln Phe Gln Leu Arg Ala Leu Met Gln Lys Ala Arg Lys Thr Ala
      370   375   380
Gly Leu Ser Asp Leu Tyr
385   390

<210> 5
<211> 27
<212> RNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
aggucaugau uguggguauuu ggagaug   27

<210> 6
<211> 27
<212> RNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
caucuccaaa uaccacaauc augaccu   27

<210> 7
<211> 39
<212> RNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
caucaucauc augaggguggc uuaugaguau uucuuccag   39

<210> 8
<211> 39
<212> RNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 8
cuacuacuac uacaccuuuu gagcaaguuc agccugguu   39

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
ctgataccag ctggaggttg agctcttc   28

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
atttagcagt cccaacattc agcacaaa   28

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gagaccgacc tctccgtaaa gcattctt   28

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
tagcccagtc agtcccagca cagcacag   28

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
atttagcagt cccaacattc agcacaaa   28

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
gtcttctggg tggcagtgat ggcat   25

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
cgggtgtcgg agagccagct caagaaa   27

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
ccttacccac ctggtggtcc atatcctg   28

<210> 17
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
cctccagctg gtatcagaga agtcgt   26

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
cacagtcaga cttgttgggg cttattc   27

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
His Thr His Leu Ala Met Asx Asp Ala
 1   5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<221> VARIANT
<222> 2
<223> Xaa = Any Amino Acid

<400> 20
Phe Xaa Asn Gly Ala Leu Glx Cys Tyr Ser
 1   5   10

<210> 21
<211> 380
<212> PRT
<213> Homo sapien

<400> 21
Met Val Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Glu Thr Val
 1   5   10   15
Asn Val Ile Thr Leu Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
                20   25   30
Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Met Asn Leu Thr Gly Thr
        35   40   45
Ile Pro Val Pro Tyr Arg Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu
    50   55   60
Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65   70   75   80
Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
                85   90   95
Gly Lys Ile Tyr Leu Pro Tyr Leu His Glu Trp Lys His Pro Gln Ser
                100   105   110
Asp Leu Leu Gly Leu Ile Gln Val Met Ile Val Val Phe Gly Asp Glu
        115